SEQUENCE LISTING

<110> Kalchman, Michael
Hayden, Michael R.
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Goldberg, Paul
Nicholson, Donald W.
Vaillancourt, John P.
Rasper, Dita M.

<120> APOPTOSIS MODULATORS THAT INTERACT WITH
THE HUNTINGTON'S DISEASE GENE

<130> MC010PI

<140> 09/701,205
<141> 2000-11-27

<150> PCT/US99/11743
<151> 1999-05-27

<150> 09/085,199
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<170> FastSEQ for Windows Version 4.0

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gttctgcaag gcagcctgga aacttctgcc cagtcagaag caaactgggc agccgagttc    960
gccgagctag agaaggagcg ggacagcctg gtgagtggcg cagctcatag ggaggaggaa   1020
ttatctgctc ttcggaaaga actgcaggac actcagctca aactggccag cacagaggaa   1080
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D)

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Lys Arg Val Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe
        35                  40                  45
Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile
    50                  55                  60
Pro Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp
65                  70                  75                  80
Asp Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys
                85                  90                  95
Phe Asp Asp Phe Gly Ser Ser Ser Ser Ser Asp Pro Phe Asn Phe Asn
            100                 105                 110
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
        115                 120                 125
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
    130                 135                 140
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
145                 150                 155                 160
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
                165                 170                 175
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Gln Arg
            180                 185                 190
Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg Lys
        195                 200                 205
Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr Ser
    210                 215                 220
Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu Val
225                 230                 235                 240
Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu Arg
                245                 250                 255
Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln Gly
            260                 265                 270
Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys Gln
        275                 280                 285
Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser Leu
    290                 295                 300
Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala Glu
305                 310                 315                 320
Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg Glu
                325                 330                 335
Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu Lys
            340                 345                 350
Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln Arg
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ccttntgttn tgttntcaac cgcctgcttc tgttttagca acgcagtgtt ttggtggaag    240
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cgctccagca acctgcagta cttcaagcgg ctcattcaga tcccccagct gcctgagaac    840
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cctgcagagg cctcatcccc cgacagcgag ccagtcctag agaaggatga cctcatggac    960
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tacagcgagc tggttcagaa ccacgctgac ctgctgcgga agaatgcaga ggtgaccaaa   1440
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gatcacctcc tctccacggt cacatccatt tccagctgca tcgagcaact ggagaaaagc   1980
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<213> Human

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Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
        35                  40                  45
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
    50                  55                  60
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
65                  70                  75                  80
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
                85                  90                  95
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
            100                 105                 110
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
        115                 120                 125
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
        130                 135                 140
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
145                 150                 155                 160
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
                165                 170                 175
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
            180                 185                 190
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
        195                 200                 205
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
        210                 215                 220
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
225                 230                 235                 240
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Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
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Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
            260             265             270
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
            275             280             285
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
290              295             300
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
305             310             315             320
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
            325             330             335
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
            340             345             350
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
            355             360             365
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
    370             375             380
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
385             390             395             400
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
            405             410             415
Gln Glu Leu Gly Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
            420             425             430
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
            435             440             445
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
    450             455             460
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
465             470             475             480
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
            485             490             495
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
            500             505             510
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
            515             520             525
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
            530             535             540
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
545             550             555             560
Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
            565             570             575
Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
            580             585             590
Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
    595             600             605
Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
    610             615             620
Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
625             630             635             640
Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
            645             650             655
Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
            660             665             670
Thr Cys Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
            675             680             685
Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Arg Cys Cys
    690             695             700
Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
705             710             715             720
Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
            725             730             735
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Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
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Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
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Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
    770                 775                 780
His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
785                 790                 795                 800
Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
                805                 810                 815
Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
            820                 825                 830
Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
            835                 840                 845
Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
    850                 855                 860
Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
865                 870                 875                 880
Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
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Lys Glu
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<212> PRT
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            20                  25                  30
Ala Gly Ser Trp Glu Arg Cys Pro Pro Leu Pro Pro Ala Gly Arg Leu
            35                  40                  45
Gln Gly Thr Asp His Pro Trp Gly Trp Gly Arg Leu Ala Gly Gly Gly
    50                  55                  60
Glu Arg Gly Gly Leu Trp Glu Gly Leu Ser His Ser Gln Arg Leu Ile
65                  70                  75                  80
His Leu Ile Leu Leu Ser Leu Pro Leu Leu Val Phe Gln Thr Val Ser
                85                  90                  95
Ile Asn Lys Ala Ile Asn Thr Gln Glu Val Ala Val Lys Glu Lys His
            100                 105                 110
Ala Arg Thr Cys Ile Leu Gly Thr His His Glu Lys Gly Ala Gln Thr
            115                 120                 125
Phe Trp Ser Val Val Asn Arg Leu Pro Leu Ser Ser Asn Ala Val Leu
    130                 135                 140
Cys Trp Lys Phe Cys His Val Phe His Lys Leu Leu Arg Asp Gly His
145                 150                 155                 160
Pro Asn Val Leu Lys Asp Ser Leu Arg Tyr Arg Asn Glu Leu Ser Asp
                165                 170                 175
Met Ser Arg Met Trp Gly His Leu Ser Glu Gly Tyr Gly Gln Leu Cys
            180                 185                 190
Ser Ile Tyr Leu Lys Leu Leu Arg Thr Lys Met Glu Tyr His Thr Lys
    195                 200                 205
Asn Pro Arg Phe Pro Gly Asn Leu Gln Met Ser Asp Arg Gln Leu Asp
    210                 215                 220
Glu Ala Gly Glu Ser Asp Val Asn Asn Phe Phe Gln Leu Thr Val Glu
225                 230                 235                 240
Met Phe Asp Tyr Leu Glu Cys Glu Leu Asn Leu Phe Gln Thr Val Phe
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                    245                 250                 255
Asn Ser Leu Asp Met Ser Arg Ser Val Ser Val Thr Ala Ala Gly Gln
            260             265                 270
Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Leu Asp Cys Ser His Leu
            275             280                 285
Tyr Asp Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
    290             295                 300
Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe Met Glu Gln Phe Thr
305             310                 315                 320
Lys Leu Lys Asp Leu Phe Tyr Arg Ser Ser Asn Leu Gln Tyr Phe Lys
                325             330                 335
Arg Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn Phe Leu
            340             345                 350
Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val Ile Pro
            355             360                 365
Ala Glu Ala Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys Asp Asp
    370             375                 380
Leu Met Asp Met Asp Ala Ser Gln Gln Asn Leu Phe Asp Asn Lys Phe
385             390                 395                 400
Asp Asp Ile Phe Gly Ser Ser Phe Ser Ser Asp Pro Phe Asn Phe Asn
            405             410                 415
Ser Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile Glu Arg
            420             425                 430
Leu Tyr Arg Glu Ile Ser Gly Leu Lys Ala Gln Leu Glu Asn Met Lys
            435             440                 445
Thr Glu Ser Gln Arg Val Val Leu Gln Leu Lys Gly His Val Ser Glu
    450             455                 460
Leu Glu Ala Asp Leu Ala Glu Gln Gln His Leu Arg Gln Gln Ala Ala
465             470                 475                 480
Asp Asp Cys Glu Phe Leu Arg Ala Glu Leu Asp Glu Leu Arg Arg Gln
            485             490                 495
Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Ser Glu Ile Glu Arg
            500             505                 510
Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu Lys Tyr
            515             520                 525
Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn Ala Glu
    530             535                 540
Val Thr Lys Gln Val Ser Met Ala Arg Gln Ala Gln Val Asp Leu Glu
545             550                 555                 560
Arg Glu Lys Lys Glu Leu Glu Asp Ser Leu Glu Arg Ile Ser Asp Gln
            565             570                 575
Gly Gln Arg Lys Thr Gln Glu Gln Leu Glu Val Leu Glu Ser Leu Lys
            580             585                 590
Gln Glu Leu Ala Thr Ser Gln Arg Glu Leu Gln Val Leu Gln Gly Ser
            595             600                 605
Leu Glu Thr Ser Ala Gln Ser Glu Ala Asn Trp Ala Ala Glu Phe Ala
    610             615                 620
Glu Leu Glu Lys Glu Arg Asp Ser Leu Val Ser Gly Ala Ala His Arg
625             630                 635                 640
Glu Glu Glu Leu Ser Ala Leu Arg Lys Glu Leu Gln Asp Thr Gln Leu
            645             650                 655
Lys Leu Ala Ser Thr Glu Glu Ser Met Cys Gln Leu Ala Lys Asp Gln
            660             665                 670
Arg Lys Met Leu Leu Val Gly Ser Arg Lys Ala Ala Glu Gln Val Ile
            675             680                 685
Gln Asp Ala Leu Asn Gln Leu Glu Glu Pro Pro Leu Ile Ser Cys Ala
    690             695                 700
Gly Ser Ala Asp His Leu Leu Ser Thr Val Thr Ser Ile Ser Ser Cys
705             710                 715                 720
Ile Glu Gln Leu Glu Lys Ser Trp Ser Gln Tyr Leu Ala Cys Pro Glu
            725             730                 735
Asp Ile Ser Gly Leu Leu His Ser Ile Thr Leu Leu Ala His Leu Thr
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                  740                      745                      750
    Ser Asp Ala Ile Ala His Gly Ala Thr Thr Cys Leu Arg Ala Pro Pro
            755                      760                      765
    Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Lys Gln Tyr Gly Arg Glu
        770                      775                      780
    Thr Leu Ala Tyr Leu Ala Ser Leu Glu Glu Glu Gly Ser Leu Glu Asn
    785                      790                      795                      800
    Ala Asp Ser Thr Ala Met Arg Asn Cys Leu Ser Lys Ile Lys Ala Ile
                    805                      810                      815
    Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu Glu Leu
            820                      825                      830
    Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu
        835                      840                      845
    Thr Ala Thr Ala Arg Ile Glu Glu Met Leu Ser Lys Ser Arg Ala Gly
        850                      855                      860
    Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly Cys Cys
    865                      870                      875                      880
    Thr Ser Leu Met Gln Ala Ile Gln Val Leu Ile Val Ala Ser Lys Asp
                    885                      890                      895
    Leu Gln Arg Glu Ile Val Glu Ser Gly Arg Gly Thr Ala Ser Pro Lys
            900                      905                      910
    Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala
            915                      920                      925
    Ser Lys Ala Val Gly Trp Gly Ala Thr Val Met Val Asp Ala Ala Asp
        930                      935                      940
    Leu Val Val Gln Gly Arg Gly Lys Phe Glu Glu Leu Met Val Cys Ser
    945                      950                      955                      960
    His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val
                    965                      970                      975
    Lys Ala Asp Lys Asp Ser Pro Asn Leu Ala Gln Leu Gln Gln Ala Ser
            980                      985                      990
    Arg Gly Val Asn Gln Ala Thr Ala Gly Val Val Ala Ser Thr Ile Ser
            995                      1000                     1005
    Gly Lys Ser Gln Ile Glu Glu Thr Asp Asn Met Asp Phe Ser Ser Met
        1010                     1015                     1020
    Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val Arg Val
    1025                     1030                     1035                     1040
    Leu Glu Leu Glu Asn Glu Leu Gln Lys Glu Arg Gln Lys Leu Gly Glu
                    1045                     1050                     1055
    Leu Arg Lys Lys His Tyr Glu Leu Ala Gly Val Ala Glu Gly Trp Glu
            1060                     1065                     1070
    Glu Gly Thr Glu Ala Ser Pro Pro Thr Leu Gln Glu Val Val Thr Glu
            1075                     1080                     1085
    Lys Glu
        1090
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<210> 6
<211> 3251
<212> DNA
<213> Human
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<400> 6
cggtgagctg gaggagcagc ggaagcagaa gcagaaggcc ctggtggata atgagcagct    60
ccgccacgag ctggcccagc tgagggctgc ccagctggag cgcgagcgga gccagggcct   120
gcgtgaggag gctgagagga aggccagtgc cacggaggcg cgctacaaca agctgaagga   180
aaagcacagt gagctcgtcc atgtgcacgc ggagctgctc agaaagaacg cggacacagc   240
caagcagctg acggtgacgc agcaaagcca ggaggaggtg gcgcgggtga aggagcagct   300
ggccttccag gtggagcagg tgaagcggga gtcggagttg aagctagagg agaagagcga   360
ccagcaggag aagctcaaga gggagctgga ggccaagcc ggagagctgg cccgcgcgca   420
ggaggccctg agccacacag agcagagcaa gtcggagctg agctcacggc tggacacact   480
gagtgcggag aaggatgctc tgagtggagc tgtgcggcag cgggaggcag acctgctggc   540
ggcgcagagc ctggtgcgcg agacagaggc ggcgctgagc cgggagcagc agcgcagctc   600
```

```
ccaggagcag ggcgagttgc agggccggct ggcagagagg gagtctcagg agcagggget    660
gcggcagagg ctgctggacg agcagttcgc agtgttgcgg ggcgctgctg ccgaggccgc    720
gggcatcctg caggatgccg tgagcaagct ggacgacccc ctgcacctgc gctgtaccag    780
ctccccagac tacctggtga gcagggccca ggaggccttg gatgccgtga gcaccctgga    840
ggagggccac gcccagtacc tgacctcctt ggcagacgcc tccgccctgg tggcagctct    900
gacccgcttc tcccacctgg ctgcggatac catcatcaat ggcggtgcca cctcgcacct    960
ggctcccacc gaccctgccg accgcctcat agacacctgc agggagtgcg gggcccgggc   1020
tctggagctc atggggcagc tgcaggacca gcaggctctg cggcacatgc aggccagcct   1080
ggtgcggaca cccctgcagg gcatccttca gctgggccaa gaactgaaac ccaagagcct   1140
agatgtgcgg caggaggagc tggggggccgt ggtcgacaag gagatggcgg ccacatccgc   1200
agccattgaa gatgctgtgc ggaggattga ggacatgatg aaccaggcac gccacgccag   1260
ctcgggggtg aagctggagg tgaacgagag gatcctcaac tcctgcacag acctgatgaa   1320
ggctatccgg ctcctggtga cgacatccac tagcctgcag aaggagatcg tggagagcgg   1380
caggggggca gccacgcagc aggaatttta cgccaagaac tcgcgctgga ccgaaggcct   1440
catctcggcc tccaaggctg tgggctgggg agccacacag ctggtggagg cagctgacaa   1500
ggtggtgctt cacacgggca agtatgagga gctcatcgtc tgctcccacg agatcgcagc   1560
cagcacggcc cagctggtgg cggcctccaa ggtgaaggcc aacaagcaca gcccccacct   1620
gagccgcctg caggaatgtt ctcgcacagt caatgagagg gctgccaatg tggtggcctc   1680
caccaagtca ggccaggagc agattgagga cagagacacc atggatttct ccggcctgtc   1740
cctcatcaag ctgaagaagc aggagatgga gacgcaggtg cgtgtcctgg agctggagaa   1800
gacgctggag gctgaacgca tgcggctggg ggagttgcag aagcaacact acgtgctggc   1860
tggggcatca ggcagccctg gagaggaggt ggccatccgg cccagcactg cccccgaag   1920
tgtaaccacc aagaaaccac ccctggccca gaagcccagc gtggcccca gacaggacca   1980
ccagcttgac aaaaaggatg gcatctaccc agctcaactc gtgaactact aggccccca   2040
ggggtccagc agggtggctg gtgacaggcc tgggcctctg caactgccct gacaggaccg   2100
agaggccttg cccctccacc tggtgcccaa gcctcccgcc ccaccgtctg gatcaatgtc   2160
ctcaaggccc ctggccctta ctgagcctgc agggtcctgg gccatgtggg tggtgcttct   2220
ggatgtgagt ctcttattta tctgcagaag gaactttggg gtgcagccag gacccggtag   2280
gcctgagcct caactcttca gaaaatagtg tttttaatat tcctcttcag aaaatagtgt   2340
ttttaatatt ccgagctaga gctcttcttc ctacgtttgt agtcagcaca ctgggaaacc   2400
gggccagcgc ggggctccct gccttctgca ctcctgaagg tcgtggatgg atggaaggca   2460
cacagcccgt gccggctgat gggacgaggg tcaggcatcc tgtctgtggc cttctggggc   2520
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gaggaatgtc gcccattacc tcctcaggcc ctggccctcg ggcctccgtg atgggagccc   2640
cccaggaggg gtcagatgct ggaaggggcc gctttctggg gagtgaggtg agacatagcg   2700
gcccaggcgc tgccttcact cctggagttt ccatttccag ctggaatctg cagccacccc   2760
catttcctgt tttccattcc cccgttctgg ccgcgcccca ctgcccacct gaaggggtgg   2820
tttccagccc tccggagagt gggcttggcc ctaggccctc cagctcagcc agaaaaagcc   2880
cagaaaccca ggtgctggac cagggccctc agggagggac cctgcggcta gagtgggcta   2940
ggccctggct ttgcccgtca gatttgaacg aatgtgtgtc ccttgagccc aaggagagcg   3000
gcaggagggg tgggaccagg ctgggaggac agagccagca gctgccatgc cctcctgctc   3060
cccccacccc agccctagcc ctttagcctt tcaccctgtg ctctggaaag gctaccaaat   3120
actggccaag gtcaggagga gcaaaaatga gccagcacca gcgccttggc tttgtgttag   3180
catttcctcc tgaagtgttc tgttggcaat aaaatgcact ttgactgtta aaaaaaaaa   3240
aaaaaaaaa a                                                        3251
```

<210> 7
<211> 676
<212> PRT
<213> Human

<400> 7
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Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys Gln Lys Ala Leu Val Asp
1               5                   10                  15
Asn Glu Gln Leu Arg His Glu Leu Ala Gln Leu Arg Ala Ala Gln Leu
            20                  25                  30
Glu Arg Glu Arg Ser Gln Gly Leu Arg Glu Glu Ala Glu Arg Lys Ala
        35                  40                  45
Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu Lys Glu Lys His Ser Glu
    50                  55                  60
Leu Val His Val His Ala Glu Leu Leu Arg Lys Asn Ala Asp Thr Ala
65                  70                  75                  80
```

- 9 -

```
Lys Gln Leu Thr Val Thr Gln Gln Ser Gln Glu Glu Val Ala Arg Val
                85                  90                  95
Lys Glu Gln Leu Ala Phe Gln Val Glu Gln Val Lys Arg Glu Ser Glu
            100             105             110
Leu Lys Leu Glu Glu Lys Ser Asp Gln Gln Glu Lys Leu Lys Arg Glu
            115             120             125
Leu Glu Ala Lys Ala Gly Glu Leu Ala Arg Ala Gln Glu Ala Leu Ser
    130             135             140
His Thr Glu Gln Ser Lys Ser Glu Leu Ser Ser Arg Leu Asp Thr Leu
145             150             155             160
Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala Val Arg Gln Arg Glu Ala
            165             170             175
Asp Leu Leu Ala Ala Gln Ser Leu Val Arg Glu Thr Glu Ala Ala Leu
            180             185             190
Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu Gln Gly Glu Leu Gln Gly
            195             200             205
Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln Gly Leu Arg Gln Arg Leu
    210             215             220
Leu Asp Glu Gln Phe Ala Val Leu Arg Gly Ala Ala Ala Glu Ala Ala
225             230             235             240
Gly Ile Leu Gln Asp Ala Val Ser Lys Leu Asp Asp Pro Leu His Leu
            245             250             255
Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val Ser Arg Ala Gln Glu Ala
            260             265             270
Leu Asp Ala Val Ser Thr Leu Glu Glu Gly His Ala Gln Tyr Leu Thr
    275             280             285
Ser Leu Ala Asp Ala Ser Ala Leu Val Ala Ala Leu Thr Arg Phe Ser
    290             295             300
His Leu Ala Ala Asp Thr Ile Ile Asn Gly Gly Ala Thr Ser His Leu
305             310             315             320
Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile Asp Thr Cys Arg Glu Cys
            325             330             335
Gly Ala Arg Ala Leu Glu Leu Met Gly Gln Leu Gln Asp Gln Gln Ala
            340             345             350
Leu Arg His Met Gln Ala Ser Leu Val Arg Thr Pro Leu Gln Gly Ile
            355             360             365
Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys Ser Leu Asp Val Arg Gln
    370             375             380
Glu Glu Leu Gly Ala Val Asp Lys Glu Met Ala Ala Thr Ser Ala
385             390             395             400
Ala Ile Glu Asp Ala Val Arg Arg Ile Glu Asp Met Met Asn Gln Ala
            405             410             415
Arg His Ala Ser Ser Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu
            420             425             430
Asn Ser Cys Thr Asp Leu Met Lys Ala Ile Arg Leu Leu Val Thr Thr
            435             440             445
Ser Thr Ser Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ala Ala
    450             455             460
Thr Gln Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu
465             470             475             480
Ile Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Gln Leu Val Glu
            485             490             495
Ala Ala Asp Lys Val Val Leu His Thr Gly Lys Tyr Glu Glu Leu Ile
            500             505             510
Val Cys Ser His Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala
    515             520             525
Ser Lys Val Lys Ala Asn Lys His Ser Pro His Leu Ser Arg Leu Gln
    530             535             540
Glu Cys Ser Arg Thr Val Asn Glu Arg Ala Ala Asn Val Val Ala Ser
545             550             555             560
Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp Arg Asp Thr Met Asp Phe
            565             570             575
```

- 10 -

```
Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys Gln Glu Met Glu Thr Gln
            580               585               590
Val Arg Val Leu Glu Leu Glu Lys Thr Leu Glu Ala Glu Arg Met Arg
        595               600               605
Leu Gly Glu Leu Arg Lys Gln His Tyr Val Leu Ala Gly Ala Ser Gly
        610               615               620
Ser Pro Gly Glu Glu Val Ala Ile Arg Pro Ser Thr Ala Pro Arg Ser
625               630               635               640
Val Thr Thr Lys Lys Pro Pro Leu Ala Gln Lys Pro Ser Val Ala Pro
                645               650               655
Arg Gln Asp His Gln Leu Asp Lys Lys Asp Gly Ile Tyr Pro Ala Gln
            660               665               670
Leu Val Asn Tyr
            675
```

```
<210> 8
<211> 2301
<212> DNA
<213> Mouse

<400> 8
ggcacgaggg ctcattcaga tcccccagct gcccgagaat ccacccaact tcctacgagc    60
ctcggccctg tcagagcaca tcagtcctgt ggtggtgatc ccggcagagg tgtcatcccc   120
agacagtgag cctgtcctgg agaaggatga cctcatggac atggacgcct cccagcagac   180
tttgtttgac aacaagtttg atgacgtctt tggcagctca ttgagcagcg acccttcaa    240
tttcaacaat caaaatggcg tgaacaagga cgagaaggac cacttgattg aacgcctgta   300
cagagagatc agtggactga cagggcagct ggacaacatg aagattgaga gccagcgggc   360
catgctgcag ctgaagggtc gagtgagtga gctggaggca gagctagcag agcagcagca   420
cttgggccgg caggctatgg atgactgcga gttcctgcgc actgagctgg atgaactgaa   480
gaggcagcga gaggacacgg agaaggcaca gcgacccctg actgagatag aaagaaaggc   540
ccaggctaat gaacagaggt atagcaagtt aaaagagaag tacagtgaac tggtgcagaa   600
ccatgctgac ctgctgcgga gaacgcaga ggtgaccaaa caggtgtccg tggcccggca   660
agcccaggtg gatttggaaa gagagaaaaa agagctagca gattcctttg cacgtgtaag   720
tgaccaggcc cagcggaaga ctcaagagca acaggatgtt ctagagaacc tgaagcatga   780
actggccacc agcagacagg agctgcaggt cctccacagc aacctggaaa cctctgccca   840
gtcagaagcg aaatggctga cacagatcgc cgagttggag aaggaacaag gcagcttggc   900
gactgttgca gctcagagag aggaagagtt atcagccctc cgagaccagc tggaaagcac   960
ccagatcaag ctggctgggg cccaggaatc catgtgccag caggtgaagg accagaggaa  1020
aaccctcttg gcagggatca ggaaggctgc ggagcgtgag atacaggagg cgctgagcca  1080
gcttgaggaa cccaccctca tcagctgtgc aggatccaca gatcaccttc tctccaaagt  1140
cagctccgtt tccagctgcc tcgagcaact ggaaaagaac ggcagccagt atctggcctg  1200
cccagaagat attagtgagc ttctgcactc gatcaccctg cttgcccact tgaccggtga  1260
cactgtcatc caggggagtg ccaccagcct ccgggcccca cggagccag ccgactcgtt   1320
gacggaggcc tgtaggcagt atggcagaga aaccctggcc tatctgtcct ccctggagga  1380
agagggaact gtggagaatg ctgacgtcac agcccttagg aattgcctca gcagggtcaa  1440
gacccttggc gaggagctgc tgcccagggg cctggacatc aagcaggaag agctgggtga  1500
cctggtggac aaggagatgg cagccacttc agctgccatt gaagctgcca ccacccggat  1560
agaggaaatt ctcagtaagt cccgagcagg agacacggga gtcaagctgg aggtgaatga  1620
gaggatcctg ggttccgta ccagcctgat gcaggccaca aaggtgcctc ttgtggcctc   1680
caaggacctc cagaaggaga tagtggagag tggcaggggt agtgcatccc ctaaagaatt  1740
ttacgccaag aactctcggt ggacggaagg gctgatatcc gcctccaaag ctgttggttg  1800
gggagctacc atcatggtgg atgctgctga tcttgtggtc caaggcaaag ggaagttcga  1860
ggagctgatg gtgtgttcac gcgagattgc tgccagtact gcccagctcg tggctgcatc  1920
caaggtgaaa gcgaacaagg gcagcctcaa tctgacccag ctgcagcagg cctctcgagg  1980
agtgaaccag gccacagccg ctgtggtggc ctcaaccatt tctggcaaat ctcagattga  2040
ggaaacagac agtatggact tctcaagcat gacactgacc cagatcaagc gccaggagat  2100
ggattcccag gttagggtgc tggagctgga aaatgacctg cagaaggagc gtcagaaact  2160
aggagagcta cggaagaaac actacgagct ggagggcgtg gctgagggct gggaggaagg  2220
gacagaagca tcaccgtcta ctgtccaaga agcaataccg gacaaagagt agagccaagc  2280
cgacacccca cacatcagaa a                                            2301

<210> 9
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<211> 756
<212> PRT
<213> Mouse

<400> 9
Ala Arg Gly Leu Ile Gln Ile Pro Gln Leu Pro Glu Asn Pro Pro Asn
1               5                   10                  15
Phe Leu Arg Ala Ser Ala Leu Ser Glu His Ile Ser Pro Val Val Val
            20              25                  30
Ile Pro Ala Glu Val Ser Ser Pro Asp Ser Glu Pro Val Leu Glu Lys
            35                  40                  45
Asp Asp Leu Met Asp Met Asp Ala Ser Gln Gln Thr Leu Phe Asp Asn
    50                  55                  60
Lys Phe Asp Asp Val Phe Gly Ser Ser Leu Ser Ser Asp Pro Phe Asn
65                  70                  75                  80
Phe Asn Asn Gln Asn Gly Val Asn Lys Asp Glu Lys Asp His Leu Ile
                85                  90                  95
Glu Arg Leu Tyr Arg Glu Ile Ser Gly Leu Thr Gly Gln Leu Asp Asn
            100                 105                 110
Met Lys Ile Glu Ser Gln Arg Ala Met Leu Gln Leu Lys Gly Arg Val
            115                 120                 125
Ser Glu Leu Glu Ala Glu Leu Ala Glu Gln Gln His Leu Gly Arg Gln
    130                 135                 140
Ala Met Asp Asp Cys Glu Phe Leu Arg Thr Glu Leu Asp Glu Leu Lys
145                 150                 155                 160
Arg Gln Arg Glu Asp Thr Glu Lys Ala Gln Arg Ser Leu Thr Glu Ile
                165                 170                 175
Glu Arg Lys Ala Gln Ala Asn Glu Gln Arg Tyr Ser Lys Leu Lys Glu
            180                 185                 190
Lys Tyr Ser Glu Leu Val Gln Asn His Ala Asp Leu Leu Arg Lys Asn
    195                 200                 205
Ala Glu Val Thr Lys Gln Val Ser Val Ala Arg Gln Ala Gln Val Asp
    210                 215                 220
Leu Glu Arg Glu Lys Lys Glu Leu Ala Asp Ser Phe Ala Arg Val Ser
225                 230                 235                 240
Asp Gln Ala Gln Arg Lys Thr Gln Glu Gln Gln Asp Val Leu Glu Asn
                245                 250                 255
Leu Lys His Glu Leu Ala Thr Ser Arg Gln Glu Leu Gln Val Leu His
            260                 265                 270
Ser Asn Leu Glu Thr Ser Ala Gln Ser Glu Ala Lys Trp Leu Thr Gln
    275                 280                 285
Ile Ala Glu Leu Glu Lys Glu Gln Gly Ser Leu Ala Thr Val Ala Ala
    290                 295                 300
Gln Arg Glu Glu Glu Leu Ser Ala Leu Arg Asp Gln Leu Glu Ser Thr
305                 310                 315                 320
Gln Ile Lys Leu Ala Gly Ala Gln Glu Ser Met Cys Gln Gln Val Lys
                325                 330                 335
Asp Gln Arg Lys Thr Leu Leu Ala Gly Ile Arg Lys Ala Ala Glu Arg
            340                 345                 350
Glu Ile Gln Glu Ala Leu Ser Gln Leu Glu Glu Pro Thr Leu Ile Ser
            355                 360                 365
Cys Ala Gly Ser Thr Asp His Leu Leu Ser Lys Val Ser Ser Val Ser
    370                 375                 380
Ser Cys Leu Glu Gln Leu Glu Lys Asn Gly Ser Gln Tyr Leu Ala Cys
385                 390                 395                 400
Pro Glu Asp Ile Ser Glu Leu Leu His Ser Ile Thr Leu Leu Ala His
                405                 410                 415
Leu Thr Gly Asp Thr Val Ile Gln Gly Ser Ala Thr Ser Leu Arg Ala
            420                 425                 430
Pro Pro Glu Pro Ala Asp Ser Leu Thr Glu Ala Cys Arg Gln Tyr Gly
            435                 440                 445
Arg Glu Thr Leu Ala Tyr Leu Ser Ser Leu Glu Glu Glu Gly Thr Val
```

```
              450                      455                      460
Glu Asn Ala Asp Val Thr Ala Leu Arg Asn Cys Leu Ser Arg Val Lys
465                      470                      475                      480
Thr Leu Gly Glu Glu Leu Leu Pro Arg Gly Leu Asp Ile Lys Gln Glu
                    485                      490                      495
Glu Leu Gly Asp Leu Val Asp Lys Glu Met Ala Ala Thr Ser Ala Ala
                500                      505                      510
Ile Glu Ala Ala Thr Thr Arg Ile Glu Glu Ile Leu Ser Lys Ser Arg
            515                      520                      525
Ala Gly Asp Thr Gly Val Lys Leu Glu Val Asn Glu Arg Ile Leu Gly
        530                      535                      540
Ser Cys Thr Ser Leu Met Gln Ala Ile Lys Val Leu Val Val Ala Ser
545                      550                      555                      560
Lys Asp Leu Gln Lys Glu Ile Val Glu Ser Gly Arg Gly Ser Ala Ser
                565                      570                      575
Pro Lys Glu Phe Tyr Ala Lys Asn Ser Arg Trp Thr Glu Gly Leu Ile
                580                      585                      590
Ser Ala Ser Lys Ala Val Gly Trp Gly Ala Thr Ile Met Val Asp Ala
                595                      600                      605
Ala Asp Leu Val Val Gln Gly Lys Gly Lys Phe Glu Glu Leu Met Val
            610                      615                      620
Cys Ser Arg Glu Ile Ala Ala Ser Thr Ala Gln Leu Val Ala Ala Ser
625                      630                      635                      640
Lys Val Lys Ala Asn Lys Gly Ser Leu Asn Leu Thr Gln Leu Gln Gln
                645                      650                      655
Ala Ser Arg Gly Val Asn Gln Ala Thr Ala Ala Val Val Ala Ser Thr
                660                      665                      670
Ile Ser Gly Lys Ser Gln Ile Glu Glu Thr Asp Ser Met Asp Phe Ser
                675                      680                      685
Ser Met Thr Leu Thr Gln Ile Lys Arg Gln Glu Met Asp Ser Gln Val
        690                      695                      700
Arg Val Leu Glu Leu Glu Asn Asp Leu Gln Lys Glu Arg Gln Lys Leu
705                      710                      715                      720
Gly Glu Leu Arg Lys Lys His Tyr Glu Leu Glu Gly Val Ala Glu Gly
                725                      730                      735
Trp Glu Glu Gly Thr Glu Ala Ser Pro Ser Thr Val Gln Glu Ala Ile
                740                      745                      750
Pro Asp Lys Glu
                755
```

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<210> 10
<211> 3979
<212> DNA
<213> Mouse

<400> 10
ggcacgaggc ggcgcgcggc ctccgtgtgc ctaggcttga ggcgggcggt gacgcctcat    60
tcgcgcggag ccgggccggg acacggtcgg cggcagcatg aacagcatca agaatgtgcc   120
ggcgcgggtg ctgagccgca ggccggggcca cagcctagag gccgagcgcg agcagttcga   180
caagacgcag gccatcagta tcagcaaagc catcaacagc caggaggccc cagtgaagga   240
gaagcatgcc cggcgtatca tcctgggcac gcatcatgag aagggagcct tcaccttctg   300
gtcctatgcc atcggcctgc cgctgtccag cagctccatc ctcagctgga agttctgtca   360
cgtccttcac aaggtcctcc gggacggaca ccccaacgtc ctgcatgact atcagcggta   420
ccggagcaac atacgtgaga tcggtgactt gtggggccac cttcgtgacc agtatggaca   480
cctggtgaat atctatacca aactgttgct gactaagatc tccttccacc ttaagcaccc   540
ccagtttcct gcaggcctgg aggtaacaga tgaggtgttg gagaaggcgg cgggaactga   600
tgtcaacaac attttttcagc ttaccgtgga gatgtttgac tacatggact gtgaactgaa   660
gctttctgag tcagtttttcc ggcagctcaa cacggccatc gcagtgtccc agatgtcttc   720
tggccagtgt cgcctagcgc cgctcatcca ggtcattcag gactgcagcc acctgtacca   780
ctacacagtg aagctcatgt ttaagctgca ctcctgtctc ccggcagaca ccctgcaagg   840
ccacagggat cggttccacg agcagttcca cagcctcaaa aacttcttcc gccgggcttc   900
agacatgctg tacttcaaga ggctcatcca gatcccgcgg ctgcctgagg gaccccccaa   960
```

- 13 -

```
tttcctgcgg gcttcagccc tggctgagca catcaagccg gtggtggtga ttcccgagga    1020
ggccccagag gaagaggagc ctgagaacct aattgaaatc agcagtgcgc cccctgctgg    1080
ggagccagtg gtggtggctg acctctttga tcagaccttt ggacccccca atggctccat    1140
gaaggatgac agggacctcc aaatcgagaa cttgaagaga gaggtggaga ccctccgtgc    1200
tgagctggag aagattaaga tggaggcaca gcggtacatc tcccagctga agggccaggt    1260
gaatggcctg gaggcagagc tggaggagca gcgcaagcag aagcagaagg ccctggtgga    1320
caacgagcag ctgcgccacg agctggccca gctcaaggcc ctgcagctgg agggcgcccg    1380
caaccagggc cttcgagagg aagcagagag gaaggccagt gccacggagg cacgctacag    1440
caagctgaag gagaaacaca gcgaactcat taacacgcac gccgagctgc tcaggaagaa    1500
cgcagacacg gccaagcagc tgacagtgac acagcagagc caggaggagg tggcacgggt    1560
aaaggaacag ctggccttcc agatggagca agcgaagcgt gagtctgaga tgaagatgga    1620
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<210> 11
<211> 1068
<212> PRT
<213> Mouse

<400> 11

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Met Asn Ser Ile Lys Asn Val Pro Ala Arg Val Leu Ser Arg Arg Pro
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Gly His Ser Leu Glu Ala Glu Arg Glu Gln Phe Asp Lys Thr Gln Ala
            20                  25                  30
```

```
Ile Ser Ile Ser Lys Ala Ile Asn Ser Gln Glu Ala Pro Val Lys Glu
        35              40              45
Lys His Ala Arg Arg Ile Ile Leu Gly Thr His His Glu Lys Gly Ala
    50              55              60
Phe Thr Phe Trp Ser Tyr Ala Ile Gly Leu Pro Leu Ser Ser Ser Ser
65              70              75              80
Ile Leu Ser Trp Lys Phe Cys His Val Leu His Lys Val Leu Arg Asp
                85              90              95
Gly His Pro Asn Val Leu His Asp Tyr Gln Arg Tyr Arg Ser Asn Ile
            100             105             110
Arg Glu Ile Gly Asp Leu Trp Gly His Leu Arg Asp Gln Tyr Gly His
        115             120             125
Leu Val Asn Ile Tyr Thr Lys Leu Leu Leu Thr Lys Ile Ser Phe His
    130             135             140
Leu Lys His Pro Gln Phe Pro Ala Gly Leu Glu Val Thr Asp Glu Val
145             150             155             160
Leu Glu Lys Ala Ala Gly Thr Asp Val Asn Asn Ile Phe Gln Leu Thr
            165             170             175
Val Glu Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser
        180             185             190
Val Phe Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser
    195             200             205
Gly Gln Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser
    210             215             220
His Leu Tyr His Tyr Thr Val Lys Leu Met Phe Lys Leu His Ser Cys
225             230             235             240
Leu Pro Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln
            245             250             255
Phe His Ser Leu Lys Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr
        260             265             270
Phe Lys Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn
    275             280             285
Phe Leu Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val
    290             295             300
Ile Pro Glu Glu Ala Pro Glu Glu Glu Pro Glu Asn Leu Ile Glu
305             310             315             320
Ile Ser Ser Ala Pro Pro Ala Gly Glu Pro Val Val Val Ala Asp Leu
            325             330             335
Phe Asp Gln Thr Phe Gly Pro Pro Asn Gly Ser Met Lys Asp Asp Arg
            340             345             350
Asp Leu Gln Ile Glu Asn Leu Lys Arg Glu Val Glu Thr Leu Arg Ala
        355             360             365
Glu Leu Glu Lys Ile Lys Met Glu Ala Gln Arg Tyr Ile Ser Gln Leu
    370             375             380
Lys Gly Gln Val Asn Gly Leu Glu Ala Glu Leu Glu Glu Gln Arg Lys
385             390             395             400
Gln Lys Gln Lys Ala Leu Val Asp Asn Glu Gln Leu Arg His Glu Leu
            405             410             415
Ala Gln Leu Lys Ala Leu Gln Leu Glu Gly Ala Arg Asn Gln Gly Leu
        420             425             430
Arg Glu Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Ser
        435             440             445
Lys Leu Lys Glu Lys His Ser Glu Leu Ile Asn Thr His Ala Glu Leu
    450             455             460
Leu Arg Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln
465             470             475             480
Ser Gln Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Met
            485             490             495
Glu Gln Ala Lys Arg Glu Ser Glu Met Lys Met Glu Glu Gln Ser Asp
        500             505             510
Gln Leu Glu Lys Leu Lys Arg Glu Leu Ala Ala Arg Ala Gly Glu Leu
        515             520             525
```

- 15 -

```
Ala Arg Ala Gln Glu Ala Leu Ser Arg Thr Glu Gln Ser Gly Ser Glu
    530                     535                 540
Leu Ser Ser Arg Leu Asp Thr Leu Asn Ala Glu Lys Glu Ala Leu Ser
545                     550                 555                 560
Gly Val Val Arg Gln Arg Glu Ala Glu Leu Leu Ala Ala Gln Ser Leu
                565                 570                 575
Val Arg Glu Lys Glu Glu Ala Leu Ser Gln Glu Gln Gln Arg Ser Ser
            580                 585                 590
Gln Glu Lys Gly Glu Leu Arg Gly Gln Leu Ala Glu Lys Glu Ser Gln
        595                 600                 605
Glu Gln Gly Leu Arg Gln Lys Leu Leu Asp Glu Gln Leu Ala Val Leu
    610                 615                 620
Arg Ser Ala Ala Ala Glu Ala Glu Ala Ile Leu Gln Asp Ala Val Ser
625                 630                 635                 640
Lys Leu Asp Asp Pro Leu His Leu Arg Cys Thr Ser Ser Pro Asp Tyr
                645                 650                 655
Leu Val Ser Arg Ala Gln Ala Ala Leu Asp Ser Val Ser Gly Leu Glu
            660                 665                 670
Gln Gly His Thr Gln Tyr Leu Ala Ser Ser Glu Asp Ala Ser Ala Leu
        675                 680                 685
Val Ala Ala Leu Thr Arg Phe Ser His Leu Ala Ala Asp Thr Ile Val
    690             695                 700
Asn Gly Ala Ala Thr Ser His Leu Ala Pro Thr Asp Pro Ala Asp Arg
705                 710                 715                 720
Leu Met Asp Thr Cys Arg Glu Cys Gly Ala Arg Ala Leu Glu Leu Val
            725                 730                 735
Gly Gln Leu Gln Asp Gln Thr Val Leu Arg Arg Ala Gln Pro Ser Leu
        740                 745                 750
Met Arg Ala Pro Leu Gln Gly Ile Leu Gln Leu Gly Gln Asp Leu Lys
    755                 760                 765
Pro Lys Ser Leu Asp Val Arg Gln Glu Glu Leu Gly Ala Met Val Asp
    770                 775                 780
Lys Glu Met Ala Ala Thr Ser Ala Ala Ile Glu Asp Ala Val Arg Arg
785                 790                 795                 800
Ile Glu Asp Met Met Ser Gln Ala Arg His Glu Ser Ser Gly Val Lys
            805                 810                 815
Leu Glu Val Asn Glu Arg Ile Leu Asn Ser Cys Thr Asp Leu Met Lys
        820                 825                 830
Ala Ile Arg Leu Leu Val Met Thr Ser Thr Ser Leu Gln Lys Glu Ile
        835                 840                 845
Val Glu Ser Gly Arg Gly Ala Ala Thr Gln Gln Glu Phe Tyr Ala Lys
    850                 855                 860
Asn Ser Arg Trp Thr Glu Gly Leu Ile Ser Ala Ser Lys Ala Val Gly
865                 870                 875                 880
Trp Gly Ala Thr Gln Leu Val Glu Ser Ala Asp Lys Val Val Leu His
            885                 890                 895
Met Gly Lys Tyr Glu Glu Leu Ile Val Cys Ser His Glu Ile Ala Ala
        900                 905                 910
Ser Thr Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asn Lys Asn
    915                 920                 925
Ser Pro His Leu Ser Arg Leu Gln Glu Cys Ser Arg Thr Val Asn Glu
    930                 935                 940
Arg Ala Ala Asn Val Val Ala Ser Thr Lys Ser Gly Gln Glu Gln Ile
945                 950                 955                 960
Glu Asp Arg Asp Thr Met Asp Phe Ser Gly Leu Ser Leu Ile Lys Leu
            965                 970                 975
Lys Lys Gln Glu Met Glu Thr Gln Val Arg Val Leu Glu Leu Glu Lys
        980                 985                 990
Thr Leu Glu Ala Glu Arg Val Arg Leu Gly Glu Leu Arg Lys Gln His
    995                 1000                1005
Tyr Val Leu Ala Gly Gly Met Gly Thr Pro Ser Glu Glu Glu Pro Ser
    1010                1015                1020
```

- 16 -

```
Arg Pro Ser Pro Ala Pro Arg Ser Gly Ala Thr Lys Lys Pro Pro Leu
1025              1030             1035             1040
Ala Gln Lys Pro Ser Ile Ala Pro Arg Thr Asp Asn Gln Leu Asp Lys
                 1045             1050             1055
Lys Asp Gly Val Tyr Pro Ala Gln Leu Val Asn Tyr
             1060             1065
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<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing primer

<400> 12
gaagataccc caccaaac   18

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> cDNA primer

<400> 13
gcttgacagt gtagtcataa aggtggctgc agtcc   35

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 14
ggacatgtcc agggagttga atac   24

<210> 15
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 15
cuacuacuac uacuaggcca cgcgtcgact agtacggggg ggggg   45

<210> 16
<211> 516
<212> DNA
<213> Human

<400> 16
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tctgtggaag gtttggaggg gagagagggg cagctggatg ctcttgggcc acggtcgccc        60
ctgatctctg cgcctcttcc tcctgctccg ggagaaataa tgtttccctg ggggatgaaa       120
gcatctcttt gtgcgggctt taattgccat gttgttgtgc caagggagtg agtggcggcg       180
ggaccagcag ctgggcacag ccaatgccag gcagtggtgc ccactccctc aggacgccca       240
gccagctggc tcctgggagc gctgcccacc tctgcccccca gctgggcgcc tgcaaggaac      300
```

```
cgaccacccg tggggctggg ggaggttggc tggaggagga gaaaggggcg ggctctggga    360
gggtctcagc cactctcaga ggcttattca tctcatcctc ctttccctcc cccttcttgt    420
ttttcagact gtcagcatca ataaggccat taatacgcag gaagtggctg taaaggaaaa    480
acacgccaga aatatccttt ggatgttgct tggaag                              516
```

<210> 17
<211> 193
<212> DNA
<213> Human

<400> 17
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tgttttccat aacccccct caccgtgcat actgggcacc caccatgaga aaggggcaca     60
gaccttctgg tctgttgtca accgcctgcc tctgtctagc aacccagtgc tctgctggaa    120
gttctgccat gtgttccaca aactcctccg agatggacac ccgaacgtga gttcctgggg    180
ctatggggtg gca                                                       193
```

<210> 18
<211> 104
<212> DNA
<213> Human

<400> 18
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gtgttctttt gcccctgcag gtcctgaagg actctctgag atacagaaat gaattgagtg     60
acatgagcag gatgtgggtg agtttggaga tgtactcagg agcc                     104
```

<210> 19
<211> 327
<212> DNA
<213> Human

<400> 19
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aattcctggc tgcagatctc ttgactgtta tgttcttgtt gttgactctg tttcccctcc     60
tcttcctaaa agggccacct gagcgagggg tatggccagc tgtgcagcat ctacctgaaa    120
ctgctaagaa ccaagatgga gtaccacacc aaagtgagtc tctgcggaca gttctgccgc    180
caccgccgcc tcccctgctc catcccttca gcccctccct gggctcattt gtcagctctt    240
tcaggtaata gacagcccag gcttctgagg aagtgtgcac atcatgtacc caagctgtga    300
gagaggaaag ccaccgccag gcccacg                                        327
```

<210> 20
<211> 331
<212> DNA
<213> Human

<400> 20
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gggctcaagc aatcctccca cctcggcctc ccaagtagct gggaccacag gcgtgtgcca     60
ccacgcccgg ctgagagagg gctcttcatg tcttctgccc tgactccctt cctctgcctc    120
ccttccagaa tcccaggttc ccaggcaacc tgcagatgag tgaccgccag ctggacgagg    180
ctggagaaag tgacgtgaac aacttgtaag tggctcctgc cctgagccca gggagggaga    240
aagcttttgt gaatgctgac acttctcata agggtcatgg agggcctgat gggggggaggc   300
cgtggctggg atggggacca aagcccctgg g                                   331
```

<210> 21
<211> 470
<212> DNA
<213> Human

<400> 21
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actgtcgctg tcactgttga cttcaccagg ctgcatggcc ataataccca caaggctaag     60
acttggagct ggagttgtgt gtgtgtttgc gcatgcacat gagcattgga gactggagta    120
gcgtagagcg tgggggaggg gacaggtaac agaccggcct caggctgtgg agtgtaagct    180
ctctttcctc ttgggtccag tttccagtta acagtggaga tgtttgacta cctggagtgt    240
gaactcaacc tcttccaaac aggtgagtct cttccctccc gtctaaccca ggctctcatg    300
```

```
ggaactacct aattcctagt cctcctctcc ctgcaaagtg tgcagcacaa ggggtaggaa      360
aatggagaca ttcacacccc atctctggtc tctccaaccc tcgtgcaggg agggactgaa      420
cctcttcagt atttttcttt ttaagagaca aggtctcggc cgggtgcagt                 470
```

<210> 22
<211> 565
<212> DNA
<213> Human

<400> 22
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tgaattagat gaggtaaagc acgcacagaa tcggtccttg gtgtatgttg gaccccctgcc     120
tctgcccctc tgaagaggct gcctgtaatc ccctggctct accacctttc tccctcactt      180
ttatttccta gtattcaact ccctggacat gtcccgctct gtgtccgtga cggcagcagg      240
gcagtgccgc ctcgccccgc tgatccaggt catcttggac tgcagccacc tttatgacta      300
cactgtcaag cttctcttca aactccactc ctgtgagtac cgcgggccag atcttcttac      360
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ttctcagtgc ctttggctgt ctgcttctgt tccaaaaggc cccggagctt ctgaccattg      480
tgaggataaa agagcagggc ccaggctttg gtgaccccag taaagcccct ggcttgccac      540
tcttgcgtcc agtgttacag gatct                                            565
```

<210> 23
<211> 233
<212> DNA
<213> Human

<400> 23
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gggacagctc taggccagtc gtggcccctg gcagtgctgg ccacatgccc cagggtagct       60
gggcccctcc ccctcgagag ccccgctgtg gcttccctgc cctctggtcc ccctcccctc      120
tcacactctt tccaatttct tccaggcctc ccagctgaca ccctgcaagg ccaccgggac      180
cgcttcatgg agcagtttac aaagtaagtg gttcaagtaa caggaatgga ggt             233
```

<210> 24
<211> 578
<212> DNA
<213> Human

<400> 24
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tgaatcccag caccatggag tttatctcct tgacagcctg tgcctttggg ctggggaggg       60
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ccctcaggtc cttctccacc cctaggttga aagatctgtt ctaccgctcc agcaacctgc      180
agtacttcaa gcggctcatt cagatccccc agctgcctga ggtaagcatg cccaaccaca      240
caccctcggc actgcagagg ccccaggtac tctcttaagg gccggcgggg cctggcaagc      300
aagcactatt tgaggatgtg tctccgtctt cagaacccac ccaacttcct gcgagcctca      360
gccctgtcag aacatatcag ccctgtggtg gtgatccctg cagaggcctc atccccgac       420
agcgagccag tcctagagaa ggatgacctc atggacatgg atgcctctca gcaggtgagg      480
accacttggg agagaaactt ggcctttcct ctcacctgca agtacagggg agaggctggg      540
ggagaccctg gccaaagccc attgactcta accaggtt                              578
```

<210> 25
<211> 390
<212> DNA
<213> Human

<400> 25
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aaaaaaattt aaaaaattaa acaggtctga accgtttaat tcgagaaagg gggcattctc       60
ccatatcact caactgaccc acacacagaa ttctctggct ctctgactta ttctcactcc      120
tttttggtca accacagaat ttatttgaca acaagtttga tgacatcttt ggcagttcat      180
tcagcagtga tcccttcaat ttcaacagtc aaaatggtgt gaacaaggat gagaagtgag      240
tccaagctgg gttcaagcag atggttcagg agctaagtta agccatggtc tgcctcaaaa      300
cactaaccaa agaggaattc ttaatgatac tggggcttct tagatacaga acatcttgaa      360
gggttggggg caatggctta tgcctgtaat                                       390
```
```
- 19 -
```

<210> 26
<211> 547
<212> DNA
<213> Human

<400> 26
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agctcacaat taaaaacaga gggatagaag cactatgaaa gcaaactcat tccccttctc   180
ttcccaggga ccacttaatt gagcgactat acagagagat cagtggattg aaggcacagc   240
tagaaaacat gaagactgag gtataacttg gatctgctct gccttttgcgc ttcaccaaaa   300
cacggtagat ttgaatgtta aatttgcatc acactagcca ggcacagtgg ctcacacctg   360
taatcctagc actttgggag gccaaggcag gaggattacc tgaggtcggg agttcgagac   420
cagcctgggc aacagggtga aaccccccgtc ttcaataaaa atgcaataat tagccgggtg   480
tgttggcagg cacctgtaat cccagctact cgggaagctg aggcatgaga attgcttgaa   540
cttggga   547

<210> 27
<211> 436
<212> DNA
<213> Human

<400> 27
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aggggaatca ggtatttact tggaagcatg gtaggacccg cttctccggc ccatgcccgt   180
gacccgtggc agtgggcggt tggcctcatg accggagtcc ccccacagag ccagcgggtt   240
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ctgcggcagc aggcggccga cgactgtgaa ttcctgcggg cagaactgga cgagctcagg   360
aggcagcggg aggacaccga gaaggctcag cggagcctgt ctgagataga aagtgagcgg   420
tgggtggggg cgggggg   436

<210> 28
<211> 469
<212> DNA
<213> Human

<400> 28
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ctgggtgaca gagcaagact gtctcaaaac aaaacaagga ggaccttcta gggaccctgg   120
ctcattgcaa ggaaggcaag ggtccctgct aggttagact cctcaccttg gtcctttaca   180
atacagggaa agctcaagcc aatgaacagc gatatagcaa gctaaaggag aagtacagcg   240
agctggttca gaaccacgct gacctgctgc ggaaggtaag accctcagcc cctgtcacca   300
tcctgcaggc cctgcacctc tagggagaga gcggctcagg cctgtggctt cccgggggcc   360
agcaacccct acattgatct ctaaggcatt gccgtcatct cgggaaccac accttttcag   420
gcttccttgc ctctgtgtct tgggctgtgt cctgggtgcc aatcccatg   469

<210> 29
<211> 359
<212> DNA
<213> Human

<400> 29
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ctagaaggag gatgtcctct aagcctggga tctcctggtt caagacactg ttcttctttt   120
gcagaatgca gaggtgacca aacaggtgtc catggccaga caagcccagg tagatttgga   180
acgagagaaa aaagagctgg aggattcgtt ggagcgcatc agtgaccagg ccagcggaa   240
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<210> 30

<211> 209
<212> DNA
<213> Human

<400> 30
gttgatcgct tgggacgttt ttacattttt atattctttg tcactgtcac ccagatcaga   60
gtccctctgt ttttcttctc tttcagactc aagaacagct ggaagttcta gagagcttga   120
agcaggaact tgccacaagc caacgggagc ttcaggttct gcaaggcagc ctggaaactt   180
ctgcccaggt aaatacctcc tttttttt   209

<210> 31
<211> 485
<212> DNA
<213> Human

<400> 31
cccccactgc aatcagtgtg tccccgggag ggaatcagag tggcaggtta aagagccatc   60
accttcccag tccttgcaac ccggtggtgg gttggacctc tgggaagtag ggactgttta   120
actcaaccag cgtctccctc tttccttgtg gtcacctttg cagtcagaag caaactgggc   180
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cacagagggt cacggacatg gacacgagcg agcacctgtg aattcccacc gagggcctct   360
gcgcatgcac ggaggctggg aggacccegg ggctgctgag aaggggtttg gggccttggc   420
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catga   485

<210> 32
<211> 468
<212> DNA
<213> Human

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tagaatctat gtgccagctt gccaaagacc aacgaaaaat gcttctggtg gggtccagga   180
aggctgcgga gcaggtgata caagacgccc tgaaccagct tgaagaacct cctctcatca   240
gctgcgctgg gtctgcaggt acacttgcaa ttgcccagct ggcaggggcc aggtccttac   300
agcctgagac tctgttgatg ttgaatctca tgtgagactt agctcagggg ctctcagccc   360
agcagcatgt cagcattacc ttaggggcgc ccaggcccca tcctagatca gttacatgtg   420
gaaactctgt gcattagtgc ctatacacta gtattttagt attttctt   468

<210> 33
<211> 393
<212> DNA
<213> Human

<400> 33
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tttccagctg catcgagcaa ctggagaaaa gctggagcca gtatctggcc tgcccagaag   180
gtaagaatgg ccaaggacag tctctgtcgg ctagtgatgg ccagacaggg ttcagaagca   240
cctgaatgcg gggatagtga caggtccctc tgcatcaaga aaggcatgta ggcaactcat   300
acaagaaagg catgtaggca actcataaaa cgggaggaga gggtatgaaa gtgtcaccat   360
caaccagacc tgagaaactt ctctttccaa tcc   393

<210> 34
<211> 421
<212> DNA
<213> Human

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gaaagtgtca  ccatcaacca  gacctgagaa  acttctcttt  ccaatcctgg  cagacatcag        240
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tgccaccacc  tgcctcagag  ccccacctga  gcctgccgac  tgtgagtact  ggggcatgag        360
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<210>  35
<211>  498
<212>  DNA
<213>  Human


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attgccttgt  atctccagca  ctgaccgagg  cctgtaagca  gtatggcagg  gaaaccctcg        180
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agctagttct  ttctgcactt  agaacttgat  tctagaaaga  gattgttaaa  attggaaaat        420
ctggccgggt  gcagtgattt  atgcgtgtaa  tcccagcact  ttgggaggcc  gagtcaggag        480
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<210>  36
<211>  427
<212>  DNA
<213>  Human


<400>  36
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ttcacaggag  ctcctgccca  ggggactgga  catcaagcag  gaggagctgg  gggacctggt        180
ggacaaggag  atggcggcca  cttcagctgc  tattgaaact  gccacggcca  gaatagaggt        240
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ctcattaaac  atgtcacagt  cgttcattaa  ggccatggca  accccctaag  acagaaacca        360
gaatttgcca  ggcacagtgg  ctcatgcctg  taaccccagc  accttgggag  gatcacttga        420
gtccagg                                                                     427


<210>  37
<211>  367
<212>  DNA
<213>  Human


<400>  37
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taagacatta  gtggatcctt  aatattcaag  gcacatttag  aaaccatgct  tctttttcac        180
aggagatgct  cagcaaatcc  cgagcaggag  acacaggagt  caaattggag  gtgaatgaaa        240
ggtcggtctg  agcggcatgg  tgggacctag  gggagcagga  tctgtcttcc  tgacattggt        300
ctatactttg  catacttatt  agggaattag  aggagagcag  tagcagccac  ggggaagggc        360
tgagttg                                                                     367


<210>  38
<211>  502
<212>  DNA
<213>  Human


<400>  38
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cagtgtatcc  tcgacttgtt  tgtttggcag  gatccttggt  tgctgtacca  gcctcatgca        180
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- 22 -

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agctattcag  gtgctcatcg  tggcctctaa  ggacctccag  agagagattg  tggagagcgg        240
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ctccaacgga  ctctgtgatg  ctgccgtctt  actctgtgtg  tccacctgag  tacagagcag        360
ccactcctgt  agatatcagc  agaggccctg  gggagaagtc  agagctccag  gacctcccca        420
gagggtggcc  aggcatgtgt  cccaactcca  gctcccttcg  cacaggcaga  cattgttgga        480
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<210>  39
<211>  437
<212>  DNA
<213>  Human
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gctcaataaa  aggtggctat  tactattttt  tatttcccta  gggtacagca  tcccctaaag        180
agttttatgc  caagaactct  cgatggacag  aaggacttat  ctcagcctcc  aaggctgtgg        240
gctggggagc  cactgtcatg  gtgtaagtat  ctattggtac  caagggtcct  cccatgaccc        300
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aaataaacta  ttgatcagga  agtcaatagg  accgagttta  caagggagcc  tggctctccc        420
aggggacaca  gggcagg                                                           437
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<210>  40
<211>  351
<212>  DNA
<213>  Human
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tagtccctct  tgtcgttttc  catcagggat  gcagctgatc  tggtggtaca  aggcagaggg        180
aaatttgagg  agctaatggt  gtgttctcat  gaaattgctc  ctagcacagc  ccagcttgtg        240
gctgcatcca  aggtaggacc  tggctggacc  tcctaggacg  ctggaaggcc  tggttagaga        300
gtactaggct  aggttaaaga  gtacttggct  gcgttaggca  gtacttggct  g                 351
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<210>  41
<211>  418
<212>  DNA
<213>  Human
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gccactgccg  gcgttgtggc  ctcaaccatt  tccggcaaat  cacagatcga  agagacaggt        300
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ctgtgatccc  aaccaaatcc  cacaggactg  tgtctaaatt  ctttcatatt  tttcatct         418
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<210>  42
<211>  279
<212>  DNA
<213>  Human
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<400>  42
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acagatcaaa  cgccaagaga  tggattctca  ggttagggtg  ctagagctag  aaaatgaatt        180
gcagaaggag  cgtcaaaaac  tgggagagct  tcggaaaaag  cactacgagc  ttgctggtgt        240
tgctgagggc  tgggaagaag  gtaagctgac  tcaaaggat                                 279
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<210>  43
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<211> 3715
<212> DNA
<213> Human

<400> 43
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acaagaagtt aaaaaacagc tgcatctgtt acttaagttt gtaagacagt gccctgagac   3480
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gtttaatccc agcactttgg gaggcagggg cgggtggatc acctgaggtc aggagttcaa   3600
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